

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 18, 2002, 04:47:34 ; Search time 116.57 Seconds
 (without alignments)
 534 256 Million cell updates/sec

Title: Perfect score: US-09-719-748-2

Sequence: 1 MEPKQQKVEDFYDGEELG.....TIEDIARRKAKHRRRSSTS 360

Scoring table: BLOSUM62
 Gappen 10.0 , Gapext 0.5

Searched: 562222 seqs, 172934929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SPREMBL_19;*

1: sp_archea;*
 2: sp_bacteria;*
 3: sp_fungi;*
 4: sp_human;*
 5: sp_invertebrate;*
 6: sp_mammal;*
 7: sp_micr;*
 8: sp_organelle;*
 9: sp_phage;*
 10: sp_plant;*
 11: sp_rabbit;*
 12: sp_virus;*
 13: sp_vertebrate;*
 14: sp_unclassified;*
 15: sp_rvirus;*
 16: sp_bacteriapl;*
 17: sp_archeap;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	1835	99 4	370	4	075892
2	1824	98 8	370	4	091X58
3	1764	95 6	370	11	09QY44
4	1481	80 2	303	11	08861
5	1297	70 3	1430	11	09QJF1
6	1293	67 8	1430	11	09QJF1
7	1251.5	67 8	345	11	09CV44
8	1166	63 2	454	4	043293
9	1140	61 8	448	11	054784
10	1140	61 8	448	11	088764
11	787	42 6	1435	5	044997
12	698	37 8	992	4	09C015
13	695	37 6	641	6	09Be69
14	688.5	37.3	907	13	098850
15	668.5	36.2	611	11	091X59
16	665.5	36.1	2762	5	P91255

Query Match 99.4%; Score 1835; DB 4; Length 370;
 Best Local Similarity 99.7%; Pred. No. 3.2e-125;
 Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Sequence 370 AA; MW: 09502B4ACCD2091 CRC64;

ALIGNMENTS

RESULT	1
07892	PRELIMINARY;
075892;	PRT; 370 AA.
075892;	DT 01-NOV-1998 (TREMBBLE. 08, Created)
075892;	DT 01-NOV-1998 (TREMBBLE. 08, Last sequence update)
075892;	DT 01-DEC-2001 (TREMBBLE. 19, Last annotation update)
075892;	DE DAP-KINASE RELATED PROTEIN 1.
075892;	OS Homo sapiens (Human)
075892;	OS Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
075892;	OC NCBL_TAXID=9606; [1]
075892;	RN SEQUENCE FROM N.A.
075892;	RC TISSUE=KIDNEY;
075892;	RA MEDLINE=2009438; Pubmed=10620061;
075892;	RA Inbal B., Shani G., Cohen O., Kissil J.L., Kimchi A.;
075892;	RT "Death-associated protein kinase-related protein 1, a novel Serine/threonine kinase involved in apoptosis.";
075892;	RT Mol. Cell. Biol. 20:1044-1054 (2000).
075892;	CC -1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
075892;	DR EMBL; AF052941; AAC25001.1; -.
075892;	DR HSSP; Q63450; 1A06.
075892;	DR InterPro; IPR000719; Euk_kinase.
075892;	DR InterPro; IPR002290; Ser_thr_kinase.
075892;	DR Pfam; PF00069; pkinase; 1.
075892;	DR SMART; SM00220; S_TKc; 1.
075892;	DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
075892;	DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
075892;	DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
075892;	DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

ID	043293	PRELIMINARY;	PRN;	454 AA.
AC	054784;			
ID	043293;	Created)		
AC	043293;	06, Last sequence update)		
DT	01-JUN-1998 (TREMBlrel. 06,			
DT	01-JUN-1998 (TREMBlrel. 06,			
DT	01-JUN-1998 (TREMBlrel. 06,			
DT	01-JUN-1998 (TREMBlrel. 06,			
DT	01-OCT-2001 (TREMBlrel. 18,	Last annotation update)		
DE	ZIP-KINASE.			
GN	ZIPK.			
OS	Homo sapiens (Human).			
OS	Bukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC	NCBI_Taxid=9606;			
RN	[1] RP SEQUENCE FROM N.A.			
RX	MEDLINE=98147805; PubMed=9488481;			
RA	Kawai T., Matsumoto M., Takeda K., Sanjo H., Akira S.;			
RA	"ZIP kinase, a novel serine/threonine kinase which mediates			
RT	"ZIP kinase, a novel serine/threonine kinase which mediates			
RT	"ZIP kinase, a novel serine/threonine kinase which mediates			
RT	"ZIP kinase, a novel serine/threonine kinase which mediates			
Mol. Cell. Biol. 18:1642-1651(1998).				
RN	[2] RP SEQUENCE FROM N.A.			
RX	MEDLINE=99283879; PubMed=10356987;			
RA	Murata-Hori M., Suizu F., Iwasaki T., Kikuchi A., Hosoya H.;			
RA	"ZIP kinase identified as a novel myosin regulatory light chain kinase			
RT	"ZIP kinase identified as a novel myosin regulatory light chain kinase			
RT	"ZIP kinase identified as a novel myosin regulatory light chain kinase			
RT	"ZIP kinase identified as a novel myosin regulatory light chain kinase			
FEBS Lett. 345: 81-84(1999).				
RL	[1] SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
CC	EMBL; AB00144; BAA24955.1. -.			
DR	EMBL; AB022341; BAA81746.1. -.			
DR	HSSP; 063450; 1A06.			
DR	InterPro; IPR002290; Ser_thr_pk kinase.			
DR	PFAM; PF00069; Pkinase_1.			
DR	SMART; SM00220; S_TKc.			
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.			
KW	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.			
SQ	SEQUENCE 454 AA; 52535 MW; 56773008A6A61FC0 CRC64;			
Query Match	63.2%; Score 1166; DB 4; Length 454;			
Best Local Similarity	64.7%; Pred. NO. 1; 3e-76;			
Matches	233; Conservative			
Matches	225; Conservative			
Matches	38; Mismatches 42; Indels 12; Gaps 3;			
Qy	1 MEPPKQOKVQVEDYDYGIGELGSQFATVKKCREKSTGLEYAAKTIKKRQSRASRRGVSR 60			
Db	1 MSTFQRODVEDHMEGMGELGSQFATVRKCOOKGTGMEYAAKFKRRLPSSRRGVSR 60			
Qy	61 IEREVSTLROVHNVITLHDYENRDTWHLTEVLEVLSGELEDPLAKESLSSEEAIFI 120			
Db	61 IEREVSTLREIRHNPNTLHDYENRDTWHLTEVLEVLSGELEDPLAKESLSSEEAIFI 120			
Qy	61 IEREVSTLROVHNVITLHDYENRDTWHLTEVLEVLSGELEDPLAKESLSSEEAIFI 120			
Db	61 IEREVNTLREIRHNPNTLHDYENRDTWHLTEVLEVLSGELEDPLAKESLSSEEAIFI 120			
Qy	121 KQILDGVNYLHTKKIAHFDLKPENIMLKDKNIPHIKLIDGKLAHETEDGVYEFKNIFGT 180			
Db	121 KQILDGVNYLHTKKIAHFDLKPENIMLKDKNIPHIKLIDGKLAHETEDGVYEFKNIFGT 180			
Qy	121 KQILDGVNYLHTKKIAHFDLKPENIMLKDKNIPHIKLIDGKLAHETEDGVYEFKNIFGT 180			
Db	121 KQILDGVNYLHTKKIAHFDLKPENIMLKDKNIPHIKLIDGKLAHETEDGVYEFKNIFGT 180			
Qy	181 PEFVAPVPIVNEYPLGLRADMWNSIGVITYILISGASPLFGLDTKQETLTANITSYDFDEEF 240			
Db	181 PEFVAPVPIVNEYPLGLRADMWNSIGVITYILISGASPLFGLDTKQETLTANITSYDFDEEF 240			
Qy	241 FSHTSELAKDFIRKLKVYKETRKRLTQBALRHPWITPVNDQAMWRSVNVLENFRQY 300			
Db	241 FSHTSELAKDFIRKLKVYKETRKRLTQBALRHPWITPVNDQAMWRSVNVLENFRQY 300			
Qy	241 FSHTSELAKDFIRKLKVYKETRKRLTQBALRHPWITPVNDQAMWRSVNVLENFRQY 300			
Db	241 FSHTSELAKDFIRKLKVYKETRKRLTQBALRHPWITPVNDQAMWRSVNVLENFRQY 300			
RESULT	10			
ID	088764	PRELIMINARY;	PRN;	448 AA.
AC	088764;			
DT	01-NOV-1998 (TREMBlrel. 08, Created)			
DT	01-NOV-1998 (TREMBlrel. 08, Last sequence update)			
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)			
DE	DAP-LIKE KINASE.			
GN	DAP-LIKE KINASE.			
OS	Rattus norvegicus (Rat).			
OC	Bukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciuropoathi; Muridae; Murinae; Rattus.			
OC	NCBI_Taxid=10090;			
RN	[1] RP SEQUENCE FROM N.A.			
RX	MEDLINE=98147805; PubMed=9488481;			
RA	Kawai T., Matsumoto M., Takeda K., Sanjo H., Akira S.;			
RA	"ZIP kinase, a novel serine/threonine kinase which mediates			
RT	"ZIP kinase, a novel serine/threonine kinase which mediates			
RT	"ZIP kinase, a novel serine/threonine kinase which mediates			
RT	"ZIP kinase, a novel serine/threonine kinase which mediates			
Mol. Cell. Biol. 18:1642-1651(1998).				
DR	HSSP; 063450; 1A06.			
DR	MGD; MGI:1203520; Dapk3.			
DR	InterPro; IPR002290; Ser_thr_pk kinase.			
DR	InterPro; IPR002290; Ser_thr_pk kinase.			
DR	PFAM; PF00069; Pkinase_1.			
DR	SMART; SM00220; S_TKc.			
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.			
KW	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.			
SQ	SEQUENCE 448 AA; 51421 MW; DA32F3EB1F20EFC CRC64;			
Query Match	61.8%; Score 1140; DB 11; Length 448;			
Best Local Similarity	71.0%; Pred. NO. 9; 7e-75;			
Matches	225; Conservative			
Matches	38; Mismatches 42; Indels 12; Gaps 3;			
Qy	1 MEPPKQOKVQVEDYDYGIGELGSQFATVKKCREKSTGLEYAAKTIKKRQSRASRRGVSR 60			
Db	1 MSTFQRODVEDHMEGMGELGSQFATVRKCOOKGTGMEYAAKFKRRLPSSRRGVSR 60			
Qy	61 IEREVSTLROVHNVITLHDYENRDTWHLTEVLEVLSGELEDPLAKESLSSEEAIFI 120			
Db	61 IEREVSTLREIRHNPNTLHDYENRDTWHLTEVLEVLSGELEDPLAKESLSSEEAIFI 120			
Qy	61 IEREVSTLROVHNVITLHDYENRDTWHLTEVLEVLSGELEDPLAKESLSSEEAIFI 120			
Db	61 IEREVNTLREIRHNPNTLHDYENRDTWHLTEVLEVLSGELEDPLAKESLSSEEAIFI 120			
Qy	121 KQILDGVNYLHTKKIAHFDLKPENIMLKDKNIPHIKLIDGKLAHETEDGVYEFKNIFGT 180			
Db	121 KQILDGVNYLHTKKIAHFDLKPENIMLKDKNIPHIKLIDGKLAHETEDGVYEFKNIFGT 180			
Qy	121 KQILDGVNYLHTKKIAHFDLKPENIMLKDKNIPHIKLIDGKLAHETEDGVYEFKNIFGT 180			
Db	121 KQILDGVNYLHTKKIAHFDLKPENIMLKDKNIPHIKLIDGKLAHETEDGVYEFKNIFGT 180			
Qy	181 PEFVAPVPIVNEYPLGLRADMWNSIGVITYILISGASPLFGLDTKQETLTANITSYDFDEEF 240			
Db	181 PEFVAPVPIVNEYPLGLRADMWNSIGVITYILISGASPLFGLDTKQETLTANITSYDFDEEF 240			
Qy	241 FSHTSELAKDFIRKLKVYKETRKRLTQBALRHPWITPVNDQAMWRSVNVLENFRQY 300			
Db	241 FSHTSELAKDFIRKLKVYKETRKRLTQBALRHPWITPVNDQAMWRSVNVLENFRQY 300			
Qy	241 FSHTSELAKDFIRKLKVYKETRKRLTQBALRHPWITPVNDQAMWRSVNVLENFRQY 300			
Db	241 FSHTSELAKDFIRKLKVYKETRKRLTQBALRHPWITPVNDQAMWRSVNVLENFRQY 300			
RESULT	9			
ID	054784	PRELIMINARY;	PRN;	448 AA.

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TAXID=9606;
 [1] RN
 RP SEQUENCE FROM N.A.
 RA Kituchi A., Murata-Hori M., Hosoya H.;
 RT "HeLa myosin light chain kinase.",
 RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 EMBL: AB037663; BAB21504.1; -.
 HSSP: P56276; ITLK.
 DR InterPro: IPR00719; Euk-pk kinase.
 DR InterPro: IPR003962; Fnnl_repeat.
 DR InterPro: IPR003961; FNIII.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR002290; Ser-thr_pk kinase.
 DR InterPro: IPR002295; Tyr_pk kinase.
 DR Pfam: PF00041; fn3; 1.
 DR Pfam: PF00047; Ig; 2.
 DR PRINTS; PR0014; FN1PEI1.
 DR SMART; SN00060; FN3; 1.
 DR SMART; SN00049; Ig; 3.
 DR SMART; SN00408; IgG2; 3.
 DR SMART; SN00220; S_TKC; 1.
 DR SMART; SN00219; TYRK; 1.
 DR PROSITE; S00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50018; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Immunoglobulin domain; Kinase; Repeat;
 KW Serine/threonine-protein kinase; Transferase.
 SEQUENCE 992 AA; 110185 MW; 3A8D772460983269 CRC64;

Query Match 37.8%; Score 698; DB 4; Length 992;
 Best Local Similarity 41.6%; Pred. No. 3e-42; Indels 22; Gaps 6;
 Matches 146; Conservative 66; Mismatches 117; Indels 22; Gaps 6;

OY 6 QKVEDFYDGEELGSGQFAIKKRCRKSTGILYAAFKIKRQSRSRSGVSRREIEREV 65
 DB 535 EOKVSDPFDIEERLGSGKQVRVLEKVKTRKWAGKFKEYAK-----EKENIROBI 588
 QY 66 SILRQLHHNVITLHDVYENRTDVHLEVLSSGELDFLAQKE-SLSBEEATSFQIKL 124
 DB 589 SIMCLHLHPKLVQCVDAEEKANTIVMVLIVSGGELFERIIDDEFELTERECIKYMRIS 648
 QY 125 DGVNVLHTKTAHFDLKPENIMLIDKNIPHIKULIDPLGLAHELEDGEVFKNIFGTPEV 184
 DB 649 EGVEYIHKOGIVHDLKPKENIMCVKNT--GTRKLIDFGLARRLENAGSLKVLFQTPERV 706
 QY 185 APEIVNVEPLGLEDADMWSGIVTYILLSGASPEFGDTKETLANTISYSYDDEFFSHT 244
 DB 707 APEIVNVEPLGIVYDAMWSGIVCIVLVLQSGLSPFMGDNNETLANTVSAWDFDEAFB1 766
 QY 245 SELAKDFIRKLKVETRKRLTQEARLHRPWI-TPVNDQAMRRESVNLNENFRQYRR 303
 DB 767 SDDAKDFISNLKKDKMKNLDCQCLQHPLMKDTKMEA---KKLSKDRMKYMAR 821
 QY 304 RWKLFSIVSLCNHLTRSLM-----KKVHLRDEDLRNCESDTEEDIAR 347
 DB 822 KWQKTNAYRAIGRLSSMAMISGLSGRSSTSPLNAEKELESEEDVSO 872
 RESULT 13
 Q9B869 PRELIMINARY; PRT; 641 AA.
 AC Q9B869;
 DT 01-JUN-2001 (TREMBrel. 17, Created)
 DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE HYPOTHETICAL 72.2 KDa PROTEIN.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC [1] RN
 RP SEQUENCE FROM N.A.
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT "Isolation of full-length cDNA clones from macaque brain cDNA
 libraries";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 EMBL: AB056801; BAB39325.1; -.
 HSSP: P56276; ITLK.
 DR InterPro: IPR000719; Euk-pk kinase.
 DR InterPro: IPR003962; Fnnl_repeat.
 DR InterPro: IPR003961; FNIII.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003600; Ig_like.
 DR InterPro: IPR002290; Ser-thr_pk kinase.
 DR InterPro: IPR001245; Tyr_pk kinase.
 DR Pfam: PF00041; fn3; 1.
 DR PRINTS; PR00014; FN1PEI1.
 DR SMART; SN00060; FN3; 1.
 DR SMART; SN00409; Ig; 1.
 DR SMART; SN00410; Ig_like; 1.
 DR SMART; SN00220; S_TKC; 1.
 DR SMART; PS00219; TYRK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50018; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Hypothetical protein; Repeat;
 KW Serine/threonine-protein kinase; Transferase.
 SEQUENCE 641 AA; 72195 MW; 488A0621858868E CRC64;

Query Match 37.6%; Score 695; DB 6; Length 641;
 Best Local Similarity 41.6%; Pred. No. 2.8e42; Indels 22; Gaps 6;
 Matches 146; Conservative 65; Mismatches 118; Indels 22; Gaps 6;

QY 6 QKVEDFYDGEELGSGQFAIKKRCRKSTGILYAAFKIKRQSRSRSGVSRREIEREV 65
 DB 257 EOKVSDPFDIEERLGSGKQVRVLEKVKTRKWAGKFKEYAK-----EKENIROBI 310
 QY 66 SILRQLHHNVITLHDVYENRTDVHLEVLSSGELDFLAQKE-SLSBEEATSFQIKL 124
 DB 311 SIMCLHLHPKLVQCVDAEEKANTIVMVLIVSGGELFERIIDDEFELTERECIKYRDIS 370
 QY 125 DGVNVLHTKTAHFDLKPENIMLIDKNIPHIKULIDPLGLAHELEDGEVFKNIFGTPEV 184
 DB 371 EGVEYIHKOGIVHDLKPKENIMCVKNT--GTRKLIDFGLARRLENAGSLKVLFQTPERV 428
 QY 185 APEIVNVEPLGLEDADMWSGIVTYILLSGASPEFGDTKETLANTISYSYDDEFFSHT 244
 DB 429 APEIVNVEPLGIVYDAMWSGIVCIVLVLQSGLSPFMGDNNETLANTVSAWDFDEAFB1 488
 QY 245 SELAKDFIRKLKVETRKRLTQEARLHRPWI-TPVNDQAMRRESVNLNENFRQYRR 303
 DB 489 SDDAKDFISNLKKDKMKNLDCQCLQHPLMKDTKMEA---KKLSKDRMKYMAR 543
 QY 304 RWKLFSIVSLCNHLTRSLM-----KKVHLRDEDLRNCESDTEEDIAR 347
 DB 544 KWQKTNAYRAIGRLSSMAMISGLSGRSSTSPLNAEKELESEEDVSO 594
 RESULT 14
 Q9B850 PRELIMINARY; PRT; 907 AA.
 ID Q9B850
 AC Q9B850;
 DT 01-FEB-1997 (TREMBrel. 02, Created)
 DT 01-FEB-1997 (TREMBrel. 02, Last sequence update)

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